FIGURE 1

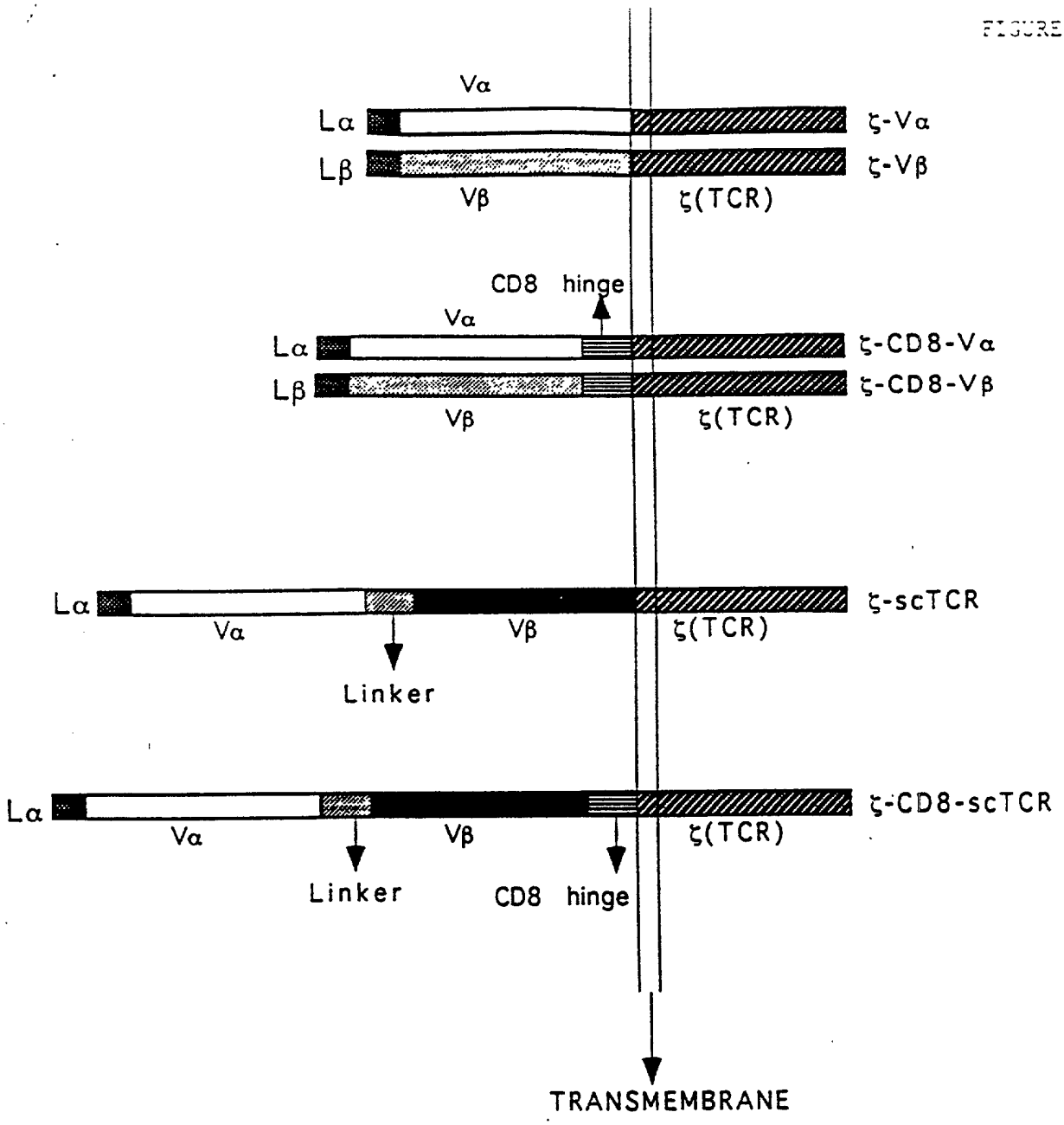
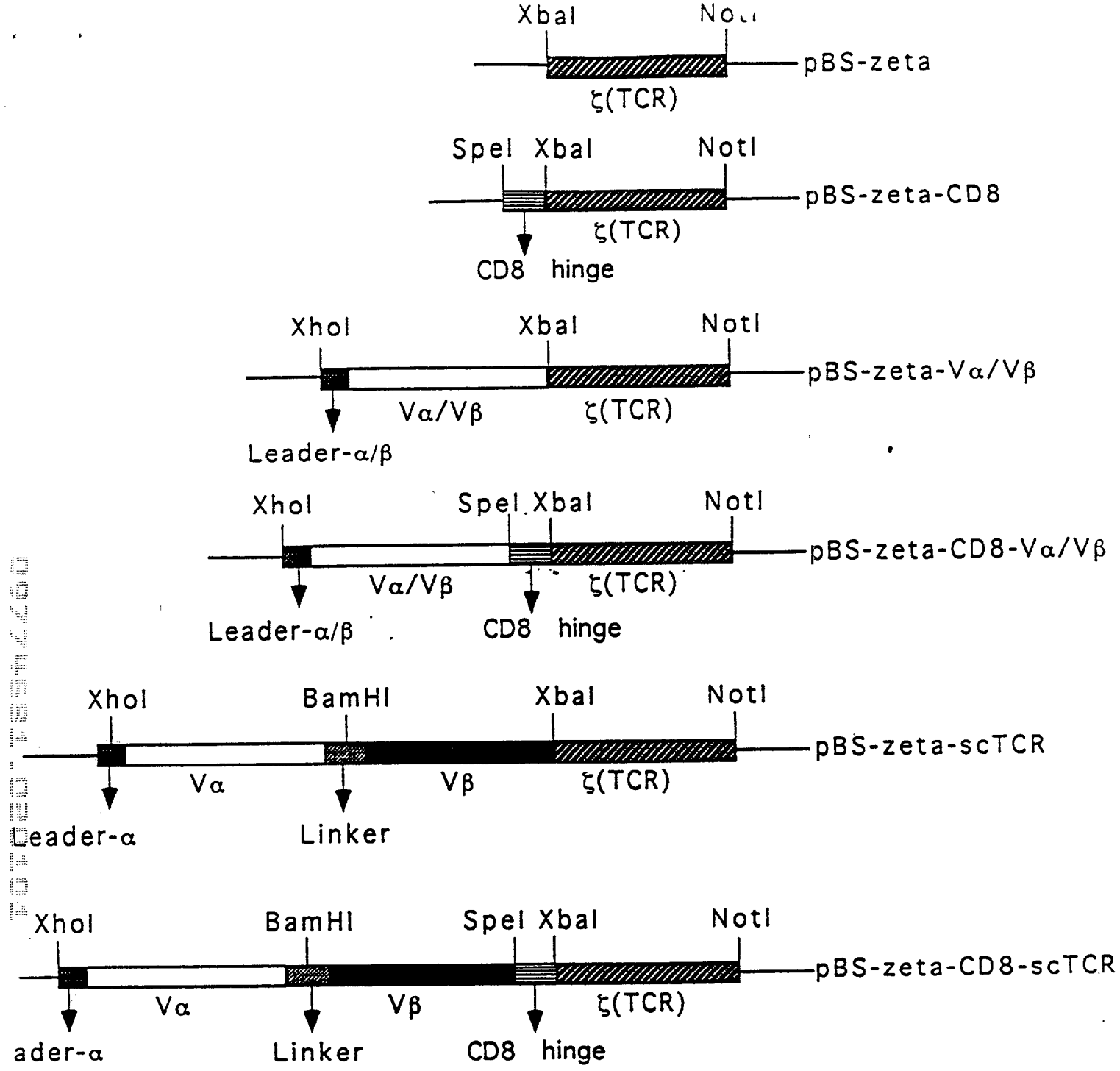

Vα
Lα
ζ-Vα
Lβ
ζ-Vβ
Vβ
ζ(TCR)
CD8 hinge
Vα
Lα
ζ-CD8-Vα
Lβ
ζ-CD8-Vβ
Vβ
ζ(TCR)
Lα
ζ-scTCR
Vα
Vβ
ζ(TCR)
Linker
Lα
ζ-CD8-scTCR
Vα
Vβ
ζ(TCR)
Linker
CD8 hinge
TRANSMEMBRANE

FIGURE 2


XbaI
NotI
pBS-zeta
ζ(TCR)
SpeI
XbaI
NotI
pBS-zeta-CD8
ζ(TCR)
CD8 hinge
XhoI
XbaI
NotI
pBS-zeta-Vα/Vβ
Vα/Vβ
ζ(TCR)
Leader-α/β
XhoI
SpeI
XbaI
NotI
pBS-zeta-CD8-Vα/Vβ
Vα/Vβ
ζ(TCR)
Leader-α/β
CD8 hinge
XhoI
BamHI
XbaI
NotI
pBS-zeta-scTCR
Vα
Vβ
ζ(TCR)
Leader-α
Linker
XhoI
BamHI
SpeI
XbaI
NotI
pBS-zeta-CD8-scTCR
Vα
Vβ
ζ(TCR)
ader-α
Linker
CD8 hinge

n Table : Universal

FIGURE 3A

LA

XhoI

```
                9                  18                  27                  36                  45                  54
CTC GAG ATG CAG AGG AAC CTG GGA GCT GTG CTG GGG ATT CTG TGG GTG CAG ATT
--- --- --- --- --- --- --- --- --- --- --- --- --- --- --- --- --- ---
 L   E   M   Q   R   N   L   G   A   V   L   G   I   L   W   V   Q   I

               63                  72                  81                  90                  99                 108
TGC TGG CTG AAA GAA CAG CAA GTG CAG CAG AGT CCC GCA TCC TTG GTT CTG CAG
--- --- --- --- --- --- --- --- --- --- --- --- --- --- --- --- --- ---
 C   W   L   K   E   Q   Q   V   Q   Q   S   P   A   S   L   V   L   Q

U2

              117                 126                 135                 144                 153                 162
GAG GGG GAG AAC GCA GAG CTC CAG TGT AGC TTT TCC ATC TTT ACA AAC CAG GTG
--- --- --- --- --- --- --- --- --- --- --- --- --- --- --- --- --- ---
 E   G   E   N   A   E   L   Q   C   S   F   S   I   F   T   N   Q   V

              171                 180                 189                 198                 207                 216
CAG TGG TTT TAC CAA CGT CCT GGG GGA AGA CTC GTC AGC CTG TTG TAC AAT CCT
--- --- --- --- --- --- --- --- --- --- --- --- --- --- --- --- --- ---
 Q   W   F   Y   Q   R   P   G   G   R   L   V   S   L   L   Y   N   P

              225                 234                 243                 252                 261                 270
TCT GGG ACA AAG CAG AGT GGG AGA CTG ACA TCC ACA ACA GTC ATT AAA GAA CGT
--- --- --- --- --- --- --- --- --- --- --- --- --- --- --- --- --- ---
 S   G   T   K   Q   S   G   R   L   T   S   T   T   V   I   K   E   R

              279                 288                 297                 306                 315                 324
CGC AGC TCT TTG CAC ATT TCC TCC TCC CAG ATC ACA GAC TCA GGC ACT TAT CTC
--- --- --- --- --- --- --- --- --- --- --- --- --- --- --- --- --- ---
 R   S   S   L   H   I   S   S   S   Q   I   T   D   S   G   T   Y   L

              333                 342                 351                 360                 369                 378
TGT GCC TCA AAT TCT GGA GGA AGC AAT GCA AAG CTA ACC TTC GGG AAA GGC ACT
--- --- --- --- --- --- --- --- --- --- --- --- --- --- --- --- --- ---
 C   A   S   N   S   G   G   S   N   A   K   L   T   F   G   K   G   T

              387                 396                 405                 414                 423 Rquat           432
AAA CTC TCT GTT AAA TCA GGT GGC GGA GGG TCT GGC GGG GGT GGA TCC GGG GGT
--- --- --- --- --- --- --- --- --- --- --- --- --- --- --- --- --- ---
 K   L   S   V   K   S   G   G   G   G   S   G   G   G   G   S   G   G

                                                    LINKER

              441                 450                 459                 468                 477                 486
GGA GGC TCA GAG GCT GCA GTC ACC CAA AGC CCA AGA AAC AAG GTG GCA GTA ACA
--- --- --- --- --- --- --- --- --- --- --- --- --- --- --- --- --- ---
 G   G   S   E   A   A   V   T   Q   S   P   R   N   K   V   A   V   T

U1

              495                 504                 513                 522                 531                 540
GGA GGA AAG GTG ACA TTG AGC TGT AAT CAG ACT AAT AAC CAC AAC AAC ATG TAC
--- --- --- --- --- --- --- --- --- --- --- --- --- --- --- --- --- ---
 G   G   K   V   T   L   S   C   N   Q   T   N   N   H   N   N   M   Y

              549                 558                 567                 576                 585                 594
TGG TAT CGG CAG GAC ACG GGG CAT GGG CTG AGG CTG ATC CAT TAT TCA TAT GGT
--- --- --- --- --- --- --- --- --- --- --- --- --- --- --- --- --- ---
 W   Y   R   Q   D   T   G   H   G   L   R   L   I   H   Y   S   Y   G

              603                 612                 621                 630                 639                 648
GCT GGC AGC ACT GAG AAA GGA GAT ATC CCT GAT GGA TAC AAG GCC TCC AGA CCA
--- --- --- --- --- --- --- --- --- --- --- --- --- --- --- --- --- ---
 A   G   S   T   E   K   G   D   I   P   D   G   Y   K   A   S   R   P
```

FIGURE 3B

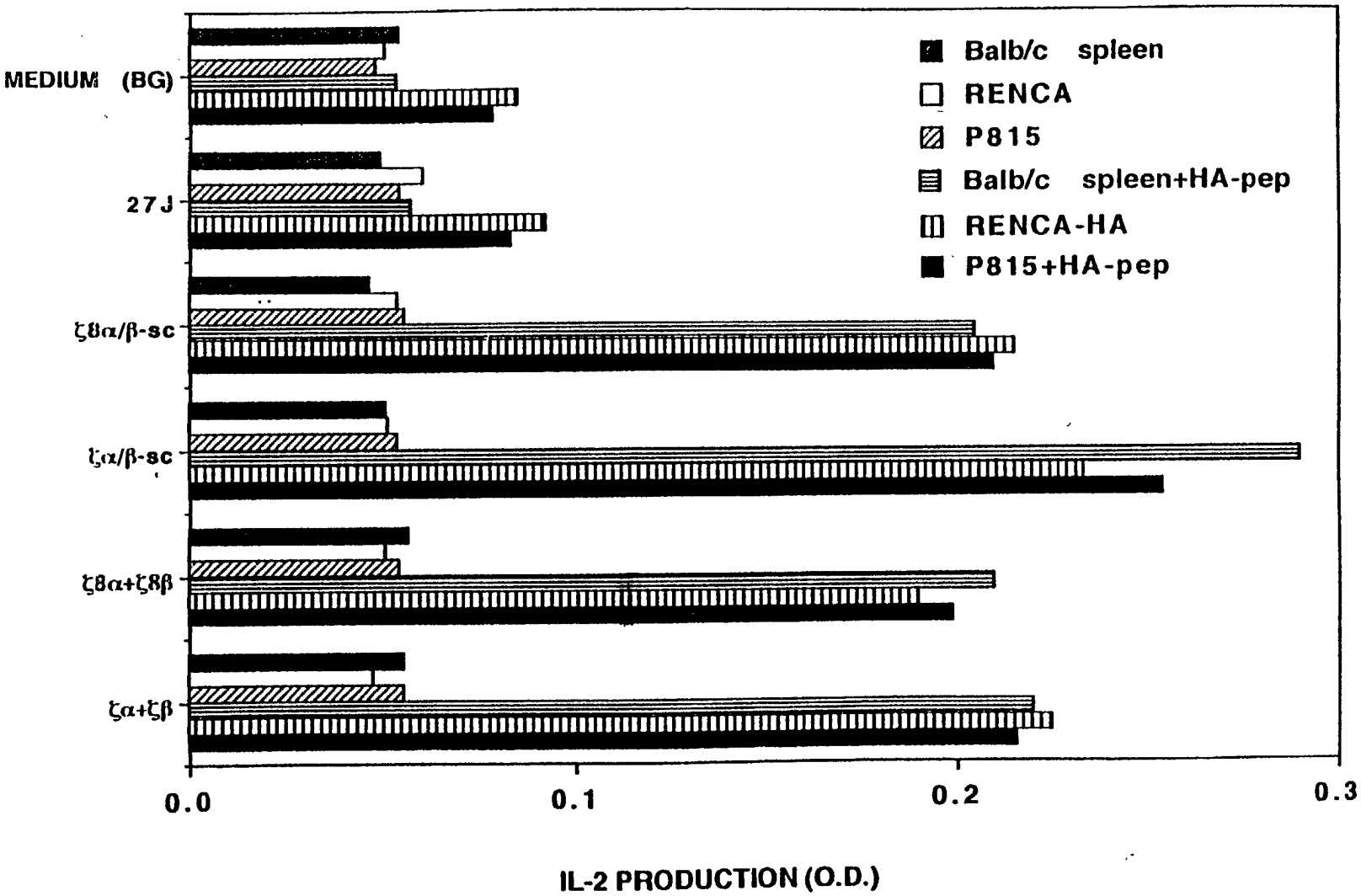
```
AGC GAA GAG AAC TTC TCC CTC ATT CTG GAG TTG GCT ACC GCC TCT GAC ACA TGA
---  ---  ---  ---  ---  ---  ---  ---  ---  ---  ---  ---  ---  ---  ---  ---  ---  ---
 S    Q    E    N    F    S    L    I    L    E    L    A    T    P    S    Q    T    S

          711            720            729            738            747            756
GTG TAC TTC TGT GCC AGC GGT GAG ACA GGG ACC AAC GAA AGA TTA TTT TTC GGT
---  ---  ---  ---  ---  ---  ---  ---  ---  ---  ---  ---  ---  ---  ---  ---  ---  ---
 V    Y    F    C    A    S    G    E    T    G    T    N    E    R    L    F    F    G

          765            774            783            792            801            810
CAT GGA ACC AAG CTG TCT GTC CTG ACT AGT AAC TCC ATC ATG TAC TTC AGC CAC
---  ---  ---  ---  ---  ---  ---  ---  ---  ---  ---  ---  ---  ---  ---  ---  ---  ---
 H    G    T    K    L    S    V    L    T    S    N    S    I    M    Y    F    S    H

          819            828            837            846            855            864
TTC GTG CCG GTC TTC CTG CCA GCG AAG CCC ACC ACG ACG CCA GCG CCG CGA CCA
---  ---  ---  ---  ---  ---  ---  ---  ---  ---  ---  ---  ---  ---  ---  ---  ---  ---
 F    V    P    V    F    L    P    A    K    P    T    T    T    P    A    P    R    P

          873            882            891            900            909            918
CCA ACA CCG GCG CCC ACC ATC GCG TCG CAG CCC CTG TCC CTG CGC CCA TCT AGT
---  ---  ---  ---  ---  ---  ---  ---  ---  ---  ---  ---  ---  ---  ---  ---  ---  ---
 P    T    P    A    P    T    I    A    S    Q    P    L    S    L    R    P    S    S

          927            936            945            954            963            972
TCT AGA GAT CCC AAA CTC TGC TAC CTG CTG GAT GGA ATC CTC TTC ATC TAT GGT
---  ---  ---  ---  ---  ---  ---  ---  ---  ---  ---  ---  ---  ---  ---  ---  ---  ---
 S    R    D    P    K    L    C    Y    L    L    D    G    I    L    F    I    Y    G

          981            990            999           1008           1017           1026
GTC ATT CTC ACT GCC TTG TTC CTG AGA GTG AAG TTC AGC AGG AGC GCA GAC GCC
---  ---  ---  ---  ---  ---  ---  ---  ---  ---  ---  ---  ---  ---  ---  ---  ---  ---
 V    I    L    T    A    L    F    L    R    V    K    F    S    R    S    A    D    A

         1035           1044           1053           1062           1071           1080
CCC GCG TAC CAG CAG GGC CAG AAC CAG CTC TAT AAC GAG CTC AAT CTA GGA CGA
---  ---  ---  ---  ---  ---  ---  ---  ---  ---  ---  ---  ---  ---  ---  ---  ---  ---
 P    A    Y    Q    Q    G    Q    N    Q    L    Y    N    E    L    N    L    G    R

         1089           1098           1107           1116           1125           1134
AGA GAG GAG TAC GAT GTT TTG GAC AAG AGA CGT GGC CGG GAC CCT GAG ATG GGG
---  ---  ---  ---  ---  ---  ---  ---  ---  ---  ---  ---  ---  ---  ---  ---  ---  ---
 R    E    E    Y    D    V    L    D    K    R    R    G    R    D    P    E    M    G

         1143           1152           1161           1170           1179           1188
GGA AAG CCG AGA AGG AAG AAC CCT CAG GAA GGC CTG TAC AAT GAA CTG CAG AAA
---  ---  ---  ---  ---  ---  ---  ---  ---  ---  ---  ---  ---  ---  ---  ---  ---  ---
 G    K    P    R    R    K    N    P    Q    E    G    L    Y    N    E    L    Q    K

         1197           1206           1215           1224           1233           1242
GAT AAG ATG GCG GAG GCC TAC AGT GAG ATT GGG ATG AAA GGC GAG CGC CGG AGG
---  ---  ---  ---  ---  ---  ---  ---  ---  ---  ---  ---  ---  ---  ---  ---  ---  ---
 D    K    M    A    E    A    Y    S    E    I    G    M    K    G    E    R    R    R

         1251           1260           1269           1278           1287           1296
GGC AAG GGG CAC GAT GGC CTT TAC CAG GGT CTC AGT ACA GCC ACC AAG GAC ACC
---  ---  ---  ---  ---  ---  ---  ---  ---  ---  ---  ---  ---  ---  ---  ---  ---  ---
 G    K    G    H    D    G    L    Y    Q    G    L    S    T    A    T    K    D    T

         1305           1314           1323           1332           1341           1350
TAC GAC GCC CTT CAC ATG CAG GCC CTG CCC CCT CGC TAA GCG GCC GCC ACC GCG
---  ---  ---  ---  ---  ---  ---  ---  ---  ---  ---  ---  ---  ---  ---  ---  ---  ---
 Y    D    A    L    H    M    Q    A    L    P    P    R    *    A    A    A    T    A
```

C H3

CD8 HINGE

2 CHAIN.

STOP



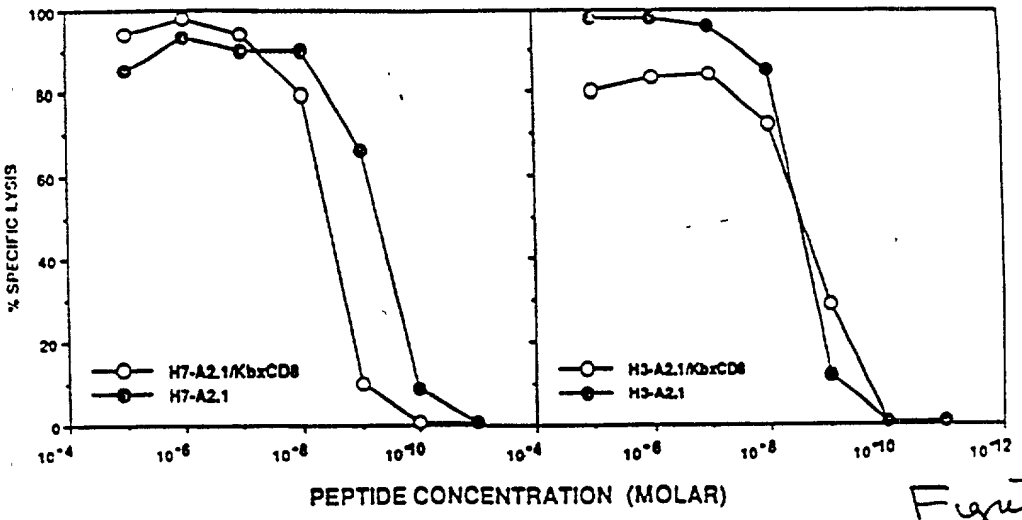

% SPECIFIC LYSIS
100
80
60
40
20
0
H7-A2.1/KbxCD8
H7-A2.1
H3-A2.1/KbxCD8
H3-A2.1
10^{-4}
10^{-6}
10^{-8}
10^{-10}
10^{-12}
PEPTIDE CONCENTRATION (MOLAR)

Figure 5

Vα1	CCC AAG GCA CTG ATG TTC ATC TTC
Vα2	TGA GAC AAA GTC CCC AAT CTC TGA CAG
Vα3	CTG CAG CTG CTC CTC AAG TAC TAT TC
Vα4.1,2,3	TCC CGG AGA AGG TCC ACA GTT CCT CTT T
Vα4.4	GAA GCA GCA GAG GGT TTG AAG CCA CAT AC

2.

Vα5	GGC AGG TCT TCA GTT GCT TAT GAA GGT
Vα6	GGT TCC TCT TCA GGG TCC AGA ATA TGT
Vα7	GCG AAG AAC TCA CCC TGG ACT GTT CAT
Vα8	GAG CTC CAC AGA CAA CAA GAG GAC CGA GCA
Vα9	GAG CTG CGA CGT TCC TTA GTG ACT GTG

3.

Vα10	CCT CGT CAG CCT GTT GTC CAA TCC TTC TGG
Vα11	CAG CCT CAT CAA TCT GTT CTA CTT GGC T
Vα12	CCA CCA GGG ACC ACA GTT TAT CAT TCA A
Vα14	ACC TGG AGA GAA TCC TAA GCT CAT CAT
Vα15	AGG TCT TGT GTC CCT GAC AGT CCT GGT T

4.

Vα16	CAA GCA AAC ACT GTA GTG CAG AGC CCT TCC
Vα17	CAA GAC ATC CAT AAC TGC CCT ACA G
Vα18	GTG TAT GAA ACC CAG GAC AGT TCT TAC
Vα19	CCG TAT TTC TTT CTT ATG TTG TTT TGG AT
Vα20	CAA AGC TCT CCA TCG CTG ACT GTT CAA G

Beta Groups

1.

Vβ1	ATC TAA TCC TGG GAA GAG CAA AT
Vβ2	GGC GTC TGG TAC CAC GTG GTC AA
Vβ3	GTG AAA GGG CAA GGA CAA AAA GC
Vβ4	GAT ATG CGA ACA GTA TCT AGG C
Vβ5.1	ACA TAA TCA AAG GAA AGG GAG AA

2.

Vβ6	TCC TGA TTG GTC AGG AAG GGC AA
Vβ7	TAC CTG ATC AAA AGA ATG GGA GA
Vβ8.1	ATA ACC ATG ACA ATA TGT ACT GG
Vβ8.2	ATA ACC ACA ACA ACA TGT ACT GG
Vβ8.3	ATA GCC ACA ACT ACA TGT ACT GG

3.

Vβ9	AGC TTG CAA GAG TTG GAA AAC CA
Vβ10	GAT TAT GTT TAG CTA CAA TAA TA
Vβ11	ACA AGG TGA CAG GGA AGG GAC AA
Vβ12	ACC TAC AGA ACC CAA GGA CTC AG
Vβ13	CAG TTG CCC TCG GAT CGA TTT TC

4.

Vβ14	GCC GAG ATC AAG GCT GTG GGC AG
Vβ15	AGA ACC ATC TGT AAG AGT GGA AC
Vβ16	CAT CAA ATA ATA GAT ATG GGG CA
Vβ17	GTA GTC CTG AAA AAG GGC ACA CT
Vβ18	CAT CTG TCA AAG TGG CAC TTC A

Range : 1 - 393 Mo : Normal
Codon Table : Universal

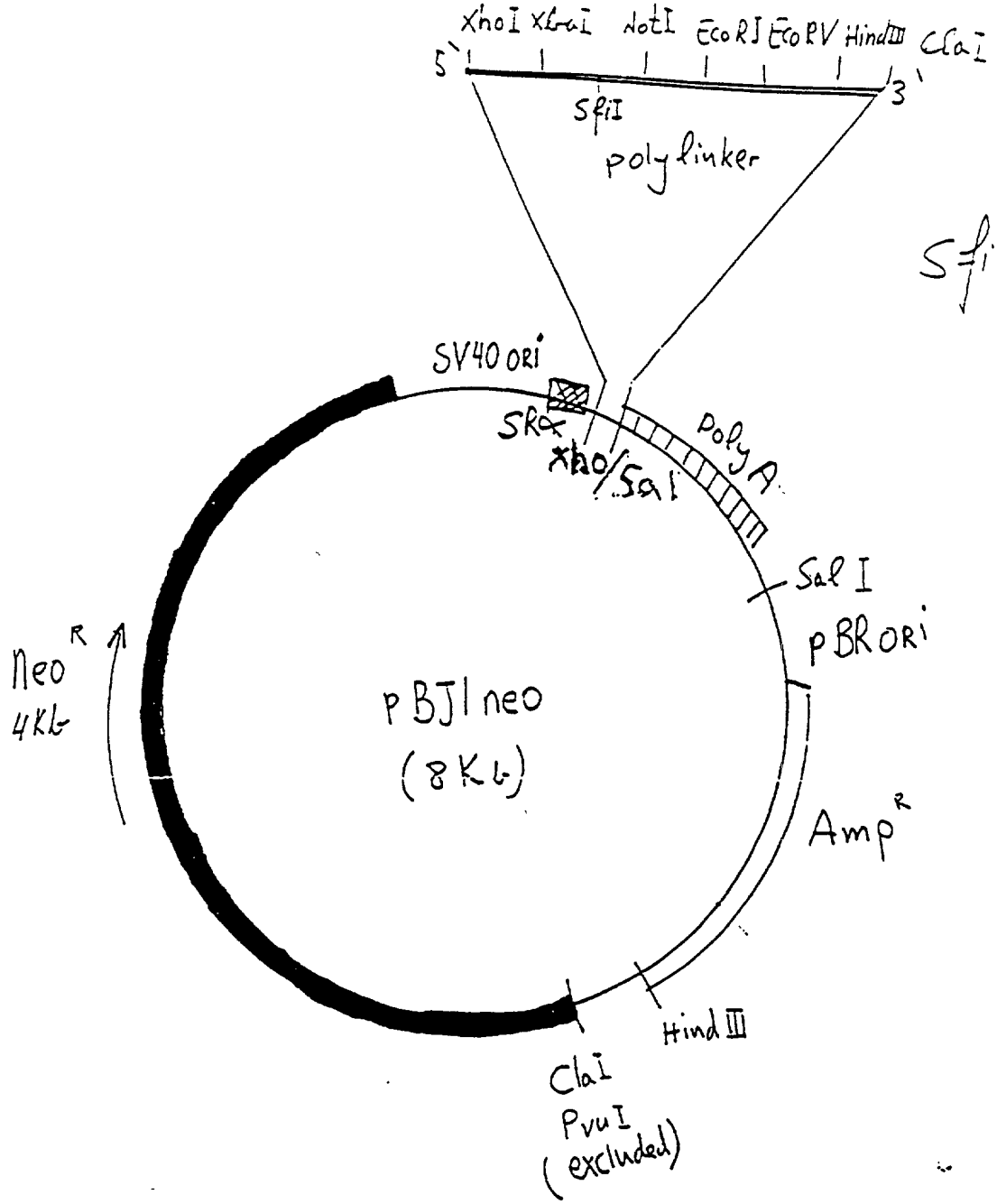
FIG. 7A

```
            9                  18                  27                  36                  45                  54
ATG AAA TCC TTG AGT GTT TCC CTA GTG GTC CTG TGG CTC CAG TTA AAC TGG GTG
--- --- --- --- --- --- --- --- --- --- --- --- --- --- --- --- --- ---
Met Lys Ser Leu Ser Val Ser Leu Val Val Leu Trp Leu Gln Leu Asn Trp Val

           63                  72                  81                  90                  99                 108
CAG AGC CAG CAG AAG GTG CAG CAG AGC CCA GAA TCC CTC AGT GTC CCA GAG GGA
--- --- --- --- --- --- --- --- --- --- --- --- --- --- --- --- --- ---
Gln Ser Gln Gln Lys Val Gln Gln Ser Pro Glu Ser Leu Ser Val Pro Glu Gly

          117                 126                 135                 144                 153                 162
GGC ATG GCC TCT CTC AAC TGC ACT TCA AGT GAT CGC AAT TTT CAG TAT TTC TGG
--- --- --- --- --- --- --- --- --- --- --- --- --- --- --- --- --- ---
Gly Met Ala Ser Leu Asn Cys Thr Ser Ser Asp Arg Asn Phe Gln Tyr Phe Trp

          171                 180                 189                 198                 207                 216
TGG TAC AGA CAG CAT TCT GGA GAA GGC CCC AAA GCA CTG ATG TCC ATC TTC TCT
--- --- --- --- --- --- --- --- --- --- --- --- --- --- --- --- --- ---
Trp Tyr Arg Gln His Ser Gly Glu Gly Pro Lys Ala Leu Met Ser Ile Phe Ser

          225                 234                 243                 252                 261                 270
GAT GGT GAC AAG AAA GAA GGC AGA TTC ACA GCT CAC CTC AAT AAG GCC AGC CTG
--- --- --- --- --- --- --- --- --- --- --- --- --- --- --- --- --- ---
Asp Gly Asp Lys Lys Glu Gly Arg Phe Thr Ala His Leu Asn Lys Ala Ser Leu

          279                 288                 297                 306                 315                 324
CAT GTT TCC CTG CAC ATC AGA GAC TCC CAG CCC AGT GAC TCC GCT CTC TAC TTC
--- --- --- --- --- --- --- --- --- --- --- --- --- --- --- --- --- ---
His Val Ser Leu His Ile Arg Asp Ser Gln Pro Ser Asp Ser Ala Leu Tyr Phe

          333                 342                 351                 360                 369                 378
TGT GCA GTT ATG GAT TAT AAC CAG GGG AAG CTT ATC TTT GGG CAG GGT ACC AAG
--- --- --- --- --- --- --- --- --- --- --- --- --- --- --- --- --- ---
Cys Ala Val Met Asp Tyr Asn Gln Gly Lys Leu Ile Phe Gly Gln Gly Thr Lys

          387
TTA TCT ATC AAG CCC 3'
--- --- --- --- ---
Leu Ser Ile Lys Pro
```

File Name : h7-beta
Range : 1 - 402 Mk : Normal
Codon Table : Universal

FIG 7B

```
           9          18          27          36          45          54
ATG GGC TCC AGA CTC TTC TTT GTG GTT TTG ATT CTC CTG TGT GCA AAA CAC ATG
--- --- --- --- --- --- --- --- --- --- --- --- --- --- --- --- --- ---
Met Gly Ser Arg Leu Phe Phe Val Val Leu Ile Leu Leu Cys Ala Lys His Met

          63          72          81          90          99         108
GAG GCT GCA GTC ACC CAA AGT CCA AGA AGC AAG GTG GCA GTA ACA GGA GGA AAG
--- --- --- --- --- --- --- --- --- --- --- --- --- --- --- --- --- ---
Glu Ala Ala Val Thr Gln Ser Pro Arg Ser Lys Val Ala Val Thr Gly Gly Lys

         117         126         135         144         153         162
GTG ACA TTG AGC TGT CAC CAG ACT AAT AAC CAT GAC TAT ATG TAC TGG TAT CGG
--- --- --- --- --- --- --- --- --- --- --- --- --- --- --- --- --- ---
Val Thr Leu Ser Cys His Gln Thr Asn Asn His Asp Tyr Met Tyr Trp Tyr Arg

         171         180         189         198         207         216
CAG GAC ACG GGG CAT GGG CTG AGG CTG ATC CAT TAC TCA TAT GTC GCT GAC AGC
--- --- --- --- --- --- --- --- --- --- --- --- --- --- --- --- --- ---
Gln Asp Thr Gly His Gly Leu Arg Leu Ile His Tyr Ser Tyr Val Ala Asp Ser

         225         234         243         252         261         270
ACG GAG AAA GGA GAT ATC CCT GAT GGG TAC AAG GCC TCC AGA CCA AGC CAA GAG
--- --- --- --- --- --- --- --- --- --- --- --- --- --- --- --- --- ---
Thr Glu Lys Gly Asp Ile Pro Asp Gly Tyr Lys Ala Ser Arg Pro Ser Gln Glu

         279         288         297         306         315         324
AAT TTC TCT CTC ATT CTG GAG TTG GCT TCC CTT TCT CAG TCA GCT GTA TAT TTC
--- --- --- --- --- --- --- --- --- --- --- --- --- --- --- --- --- ---
Asn Phe Ser Leu Ile Leu Glu Leu Ala Ser Leu Ser Gln Ser Ala Val Tyr Phe

         333         342         351         360         369         378
TGT GCC AGC AGC GAT TTC GCC GGG ACA GGG GGC TTC TAT GAA CAG TAC TTC GGT
--- --- --- --- --- --- --- --- --- --- --- --- --- --- --- --- --- ---
Cys Ala Ser Ser Asp Phe Ala Gly Thr Gly Gly Phe Tyr Glu Gln Tyr Phe Gly

         387         396
CCC GGC ACC AGG CTC ACG GTT TCT 3'
--- --- --- --- --- --- --- ---
Pro Gly Thr Arg Leu Thr Val Ser
```



SfiI - NotI

Ref:

pBJIneo - MCB 8: 466, 1988

Polylinker - Science, 249: 677, 1990

FIGURE 9

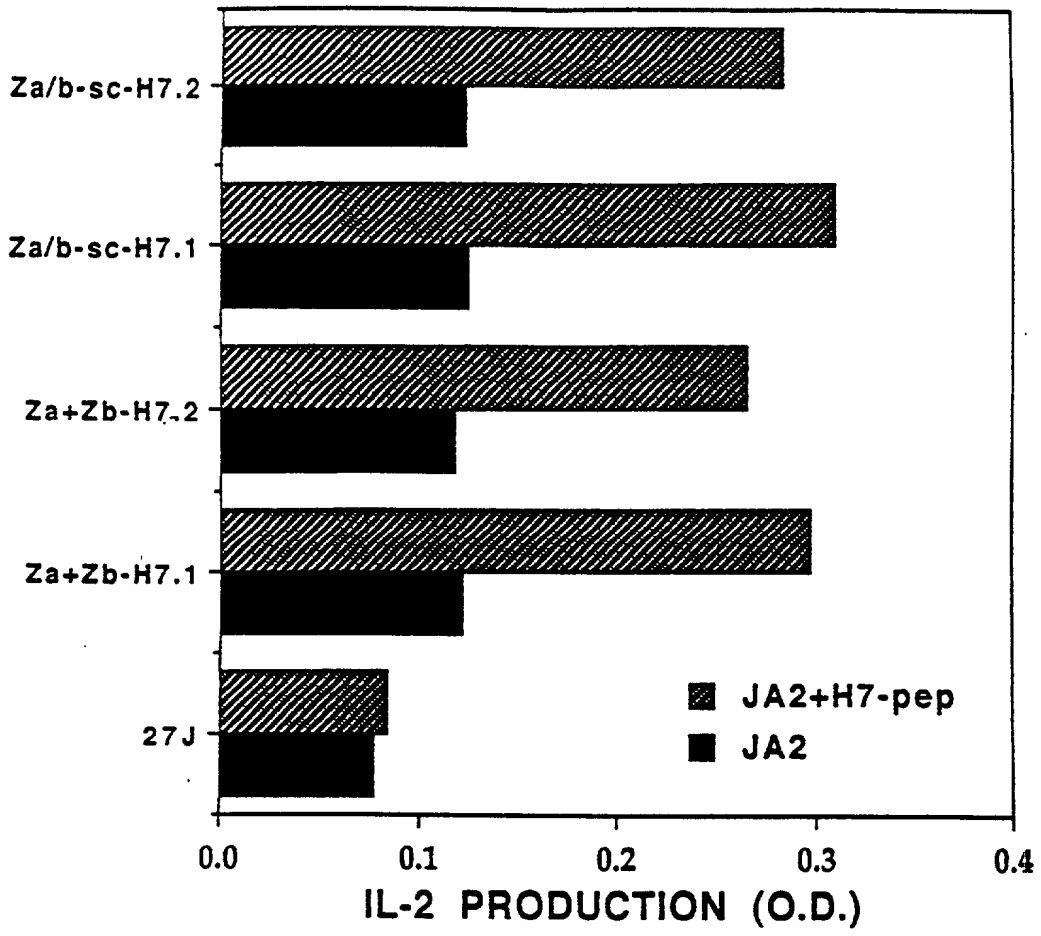

Za/b-sc-H7.2
Za/b-sc-H7.1
Za+Zb-H7.2
Za+Zb-H7.1
27J
JA2+H7-pep
JA2
0.0
0.1
0.2
0.3
0.4
IL-2 PRODUCTION (O.D.)

FIGURE 10